

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

WARREN, Patrick V.

SWANSON, Ronald V.

(ii) TITLE OF INVENTION:

TRANSAMINASES AND AMINOTRANSFERASES

(iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish and Richardson P.C.
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 INCH DISKETTE
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: WORD PERFECT 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unassigned
(B) FILING DATE: Concurrently
(C) CLASSIFICATION: Unassigned

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/599,171
(B) FILING DATE: 2/9/96
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lisa A. Haile, Ph.D.
(B) REGISTRATION NUMBER: 38,347
(C) REFERENCE/DOCKET NUMBER: 09010/016002

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-678-5070
(B) TELEFAX: 619-678-5099

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGATTGAA GACCCTATGG AC

52

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGATCT TTAAGCACTT CTCTCAGGTT C

31

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGGACAGG CTTGAAAAAG TA

52

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGATCT TCAGCTAAGC TTCTCTAAGA A

31

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGTGGGAA TTAGACCCTA AA

52

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAGGATCC CTACACCTGT TTTTCAAGCT C

31

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGACATAC TTAATGAACA AT

52

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGAAGATCT TTATGAGAAG TCCCTTTCAA G

31

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGCGGAAA CTGGCCGAGC GG

52

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGAGGATCC TTAAAGTGCC GCTTCGATCA A

31

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGTGCGGG ATAGTCGGAT AC

52

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGAAGATCT TTATTCCACC GTGACCGTTT T

31

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGATACCC CAGAGGATTA AG

52

- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGGAAGATCT TTAAAGAGAG CTTGAAAGGG A

31

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 52 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAAGCCG TACGCTAAAT AT

52

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 31 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGAAGATCT CTAATACACA GGAGTGATCC A

31

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1245 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG ATT GAA GAC CCT ATG GAC TGG GCT TTT CCG AGG ATA AAG AGA CTG
Met Ile Glu Asp Pro Met Asp Trp Ala Phe Pro Arg Ile Lys Arg Leu
5 10 15

48

CCT CAG TAT GTC TTC TCT CTC GTT AAC GAA CTC AAG TAC AAG CTA AGG
Pro Gln Tyr Val Phe Ser Leu Val Asn Glu Leu Lys Tyr Lys Leu Arg
20 25 30

96

CGT GAA GGC GAA GAT GTA GTG GAT CTT GGT ATG GGC AAT CCT AAC ATG
Arg Glu Gly Glu Asp Val Val Asp Leu Gly Met Gly Asn Pro Asn Met
35 40 45

144

CCT CCA GCA AAG CAC ATA ATA GAT AAA CTC TGC GAA GTG GCT CAA AAG
Pro Pro Ala Lys His Ile Ile Asp Lys Leu Cys Glu Val Ala Gln Lys
50 55 60

192

CCG AAC GTT CAC GGA TAT TCT GCG TCA AGG GGC ATA CCA AGA CTG AGA Pro Asn Val His Gly Tyr Ser Ala Ser Arg Gly Ile Pro Arg Leu Arg 65 70 75 80	240
AAG GCT ATA TGT AAC TTC TAC GAA GAA AGG TAC GGA GTG AAA CTC GAC Lys Ala Ile Cys Asn Phe Tyr Glu Glu Arg Tyr Gly Val Lys Leu Asp 85 90 95	288
CCT GAG AGG GAG GCT ATA CTA ACA ATC GGT GCA AAG GAA GGG TAT TCT Pro Glu Arg Glu Ala Ile Leu Thr Ile Gly Ala Lys Glu Gly Tyr Ser 100 105 110	336
CAT TTG ATG CTT GCG ATG ATA TCT CCG GGT GAT ACG GTA ATA GTT CCT His Leu Met Leu Ala Met Ile Ser Pro Gly Asp Thr Val Ile Val Pro 115 120 125	384
AAT CCC ACC TAT CCT ATT CAC TAT TAC GCT CCC ATA ATT GCA GGA GGG Asn Pro Thr Tyr Pro Ile His Tyr Tyr Ala Pro Ile Ile Ala Gly Gly 130 135 140	432
GAA GTT CAC TCA ATA CCC CTT AAC TTC TCG GAC GAT CAA GAT CAT CAG Glu Val His Ser Ile Pro Leu Asn Phe Ser Asp Asp Gln Asp His Gln 145 150 155 160	480
GAA GAG TTT TTA AGG AGG CTT TAC GAG ATA GTA AAA ACC GCG ATG CCA Glu Glu Phe Leu Arg Arg Leu Tyr Glu Ile Val Lys Thr Ala Met Pro 165 170 175	528
AAA CCC AAG GCT GTC GTC ATA AGC TTT CCT CAC AAT CCA ACG ACC ATA Lys Pro Lys Ala Val Val Ile Ser Phe Pro His Asn Pro Thr Thr Ile 180 185 190	576
ACG GTA GAA AAG GAC TTT TTT AAA GAA ATA GTT AAG TTT GCA AAG GAA Thr Val Glu Lys Asp Phe Phe Lys Glu Ile Val Lys Phe Ala Lys Glu 195 200 205	624
CAC GGT CTC TGG ATA ATA CAC GAT TTT GCG TAT GCG GAT ATA GCC TTT His Gly Leu Trp Ile Ile His Asp Phe Ala Tyr Ala Asp Ile Ala Phe 210 215 220	672
GAC GGT TAC AAG CCC CCC TCA ATA CTC GAA ATA GAA GGT GCT AAA GAC Asp Gly Tyr Lys Pro Pro Ser Ile Leu Glu Ile Glu Gly Ala Lys Asp 225 230 235 240	720
GTT GCG GTT GAG CTC TAC TCC ATG TCA AAG GGC TTT TCA ATG GCG GGC Val Ala Val Glu Leu Tyr Ser Met Ser Lys Gly Phe Ser Met Ala Gly 245 250 255	768
TGG AGG GTA GCC TTT GTC GTT GGA AAC GAA ATA CTC ATA AAA AAC CTT Trp Arg Val Ala Phe Val Val Gly Asn Glu Ile Leu Ile Lys Asn Leu 260 265 270	816
GCA CAC CTC AAA AGC TAC TTG GAT TAC GGT ATA TTT ACT CCC ATA CAG Ala His Leu Lys Ser Tyr Leu Asp Tyr Gly Ile Phe Thr Pro Ile Gln 275 280 285	864
GTG GCC TCT ATT ATC GCA TTA GAG AGC CCC TAC GAA ATC GTG GAA AAA Val Ala Ser Ile Ile Ala Leu Glu Ser Pro Tyr Glu Ile Val Glu Lys 290 295 300	912
ACC GCA AAG GTT TAC CAA AAA AGA AGA GAC GTT CTG GTG GAA GGG TTA	960

Thr	Ala	Lys	Val	Tyr	Gln	Lys	Arg	Arg	Asp	Val	Leu	Val	Glu	Gly	Leu	
305					310					315					320	
AAC	AGG	CTC	GGC	TGG	AAA	GTA	AAA	AAA	CCT	AAG	GCT	ACC	ATG	TTC	GTC	1008
Asn	Arg	Leu	Gly	Trp	Lys	Val	Lys	Lys	Pro	Lys	Ala	Thr	Met	Phe	Val	
			325						330					335		
TGG	GCA	AAG	ATT	CCC	GAA	TGG	ATA	AAT	ATG	AAC	TCT	CTG	GAC	TTT	TCC	1056
Trp	Ala	Lys	Ile	Pro	Glu	Trp	Ile	Asn	Met	Asn	Ser	Leu	Asp	Phe	Ser	
			340					345					350			
TTG	TTC	CTC	CTA	AAA	GAG	GCG	AAG	GTT	GCG	GTA	TCC	CCG	GGT	GTG	GGC	1104
Leu	Phe	Leu	Leu	Lys	Glu	Ala	Lys	Val	Ala	Val	Ser	Pro	Gly	Val	Gly	
			355				360					365				
TTT	GGT	CAG	TAC	GGA	GAG	GGG	TAC	GTA	AGG	TTT	GCA	CTT	GTA	GAA	AAT	1152
Phe	Gly	Gln	Tyr	Gly	Glu	Gly	Tyr	Val	Arg	Phe	Ala	Leu	Val	Glu	Asn	
	370					375					380					
GAA	CAC	AGG	ATC	AGA	CAG	GCT	ATA	AGG	GGA	ATA	AGG	AAA	GCC	TTC	AGA	1200
Glu	His	Arg	Ile	Arg	Gln	Ala	Ile	Arg	Gly	Ile	Arg	Lys	Ala	Phe	Arg	
385					390				395						400	
AAA	CTC	CAG	AAG	GAG	AGG	AAA	CTT	GAA	CCT	GAG	AGA	AGT	GCT	TAA		1245
Lys	Leu	Gln	Lys	Glu	Arg	Lys	Leu	Glu	Pro	Glu	Arg	Ser	Ala	End		
			405					410				414				

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1122 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG	GAC	AGG	CTT	GAA	AAA	GTA	TCA	CCC	TTC	ATA	GTA	ATG	GAT	ATC	CTA	48
Met	Asp	Arg	Leu	Glu	Lys	Val	Ser	Pro	Phe	Ile	Val	Met	Asp	Ile	Leu	
			5					10						15		
GCT	CAG	GCC	CAG	AAG	TAC	GAA	GAC	GTA	GTA	CAC	ATG	GAG	ATA	GGA	GAG	96
Ala	Gln	Ala	Gln	Lys	Tyr	Glu	Asp	Val	Val	His	Met	Glu	Ile	Gly	Glu	
			20					25					30			
CCC	GAT	TTA	GAA	CCG	TCT	CCC	AAG	GTA	ATG	GAA	GCT	CTG	GAA	CGT	GCG	144
Pro	Asp	Leu	Glu	Pro	Ser	Pro	Lys	Val	Met	Glu	Ala	Leu	Glu	Arg	Ala	
			35				40					45				
GTG	AAG	GAA	AAG	ACG	TTC	TTC	TAC	ACC	CCT	GCT	CTG	GGA	CTC	TGG	GAA	192
Val	Lys	Glu	Lys	Thr	Phe	Phe	Tyr	Thr	Pro	Ala	Leu	Gly	Leu	Trp	Glu	
	50					55					60					
CTC	AGG	GAA	AGG	ATA	TCG	GAG	TTT	TAC	AGG	AAA	AAG	TAC	AGC	GTT	GAA	240
Leu	Arg	Glu	Arg	Ile	Ser	Glu	Phe	Tyr	Arg	Lys	Lys	Tyr	Ser	Val	Glu	
	65				70				75						80	
GTT	TCT	CCA	GAG	AGA	GTC	ATC	GTA	ACT	ACC	GGA	ACT	TCG	GGA	GCG	TTT	288
Val	Ser	Pro	Glu	Arg	Val	Ile	Val	Thr	Thr	Gly	Thr	Ser	Gly	Ala	Phe	
			85					90					95			
CTC	GTA	GCC	TAC	GCC	GTA	ACA	CTA	AAT	GCG	GGA	GAG	AAG	ATA	ATC	CTC	336

Leu	Val	Ala	Tyr	Ala	Val	Thr	Leu	Asn	Ala	Gly	Glu	Lys	Ile	Ile	Leu	
			100					105					110			
CCA	GAC	CCC	TCT	TAC	CCC	TGT	TAC	AAA	AAC	TTT	GCC	TAC	CTC	TTA	GAC	384
Pro	Asp	Pro	Ser	Tyr	Pro	Cys	Tyr	Lys	Asn	Phe	Ala	Tyr	Leu	Leu	Asp	
		115					120				125					
GCT	CAG	CCG	GTT	TTC	GTA	AAC	GTT	GAC	AAG	GAA	ACG	AAT	TAC	GAA	GTA	432
Ala	Gln	Pro	Val	Phe	Val	Asn	Val	Asp	Lys	Glu	Thr	Asn	Tyr	Glu	Val	
	130					135					140					
AGG	AAA	GAG	ATG	ATA	GAA	GAC	ATT	GAT	GCG	AAA	GCC	CTT	CAC	ATT	TCC	480
Arg	Lys	Glu	Met	Ile	Glu	Asp	Ile	Asp	Ala	Lys	Ala	Leu	His	Ile	Ser	
	145				150					155					160	
TCG	CCT	CAA	AAC	CCT	ACG	GGC	ACA	CTC	TAC	TCA	CCT	GAA	ACC	CTG	AAG	528
Ser	Pro	Gln	Asn	Pro	Thr	Gly	Thr	Leu	Tyr	Ser	Pro	Glu	Thr	Leu	Lys	
				165					170					175		
GAA	CTT	GCG	GAG	TAC	TGC	GAA	GAG	AAG	GGT	ATG	TAC	TTC	ATA	TCC	GAC	576
Glu	Leu	Ala	Glu	Tyr	Cys	Glu	Glu	Lys	Gly	Met	Tyr	Phe	Ile	Ser	Asp	
			180					185					190			
GAG	ATT	TAC	CAC	GGA	CTC	GTT	TAC	GAA	GGT	AGG	GAG	CAC	ACA	GCA	CTT	624
Glu	Ile	Tyr	His	Gly	Leu	Val	Tyr	Glu	Gly	Arg	Glu	His	Thr	Ala	Leu	
		195					200					205				
GAG	TTC	TCT	GAC	AGG	GCT	ATT	GTC	ATA	AAC	GGG	TTT	TCT	AAG	TAC	TTC	672
Glu	Phe	Ser	Asp	Arg	Ala	Ile	Val	Ile	Asn	Gly	Phe	Ser	Lys	Tyr	Phe	
	210					215					220					
TGT	ATG	CCA	GGT	TTC	AGG	ATA	GGG	TGG	ATG	ATA	GTT	CCG	GAA	GAA	CTC	720
Cys	Met	Pro	Gly	Phe	Arg	Ile	Gly	Trp	Met	Ile	Val	Pro	Glu	Glu	Leu	
	225				230					235					240	
GTG	AGA	AAG	GCG	GAA	ATA	GTA	ATT	CAG	AAC	GTA	TTT	ATA	TCT	GCC	CCG	768
Val	Arg	Lys	Ala	Glu	Ile	Val	Ile	Gln	Asn	Val	Phe	Ile	Ser	Ala	Pro	
				245					250					255		
ACG	CTC	AGT	CAG	TAC	GCC	GCC	CTT	GAG	GCT	TTT	GAT	TAC	GAG	TAT	TTG	816
Thr	Leu	Ser	Gln	Tyr	Ala	Ala	Leu	Glu	Ala	Phe	Asp	Tyr	Glu	Tyr	Leu	
			260					265					270			
GAG	AAG	GTA	AGA	AAA	ACC	TTT	GAA	GAG	AGG	AGG	AAC	TTC	CTT	TAT	GGG	864
Glu	Lys	Val	Arg	Lys	Thr	Phe	Glu	Glu	Arg	Arg	Asn	Phe	Leu	Tyr	Gly	
		275					280					285				
GAA	CTG	AAA	AAA	CTC	TTC	AAG	ATA	GAC	GCG	AAA	CCT	CAG	GGA	GCT	TTT	912
Glu	Leu	Lys	Lys	Leu	Phe	Lys	Ile	Asp	Ala	Lys	Pro	Gln	Gly	Ala	Phe	
	290					295					300					
TAC	GTA	TGG	GCA	AAC	ATA	AGT	GAT	TAC	TCC	ACA	GAT	AGC	TAC	GAA	TTT	960
Tyr	Val	Trp	Ala	Asn	Ile	Ser	Asp	Tyr	Ser	Thr	Asp	Ser	Tyr	Glu	Phe	
	305				310					315					320	
GCT	TTA	AAA	CTT	TTA	AGG	GAG	GCG	AGG	GTG	GCG	GTA	ACG	CCC	GGG	GTG	1008
Ala	Leu	Lys	Leu	Leu	Arg	Glu	Ala	Arg	Val	Ala	Val	Thr	Pro	Gly	Val	
				325					330					335		
GAC	TTT	GGA	AAA	AAC	AAA	ACG	AAG	GAG	TAT	ATA	AGG	TTT	GCT	TAT	ACG	1056
Asp	Phe	Gly	Lys	Asn	Lys	Thr	Lys	Glu	Tyr	Ile	Arg	Phe	Ala	Tyr	Thr	
			340					345					350			

AGA AAG ATA GAA GAA CTT AAG GAG GGC GTT GAA AGG ATA AAG AAG TTC	1104
Arg Lys Ile Glu Glu Leu Lys Glu Gly Val Glu Arg Ile Lys Lys Phe	
355 360 365	

TTA GAG AAG CTT AGC TGA	1122
Leu Glu Lys Leu Ser End	
370	

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1359 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG TGG GAA TTA GAC CCT AAA ACG CTC GAA AAG TGG GAC AAG GAG TAC	48
Met Trp Glu Leu Asp Pro Lys Thr Leu Glu Lys Trp Asp Lys Glu Tyr	
5 10 15	
TTC TGG CAT CCA TTT ACC CAG ATG AAA GTC TAC AGA GAA GAA GAA AAC	96
Phe Trp His Pro Phe Thr Gln Met Lys Val Tyr Arg Glu Glu Glu Asn	
20 25 30	
CTG ATA TTT GAA CGC GGA GAA GGC GTT TAC CTG TGG GAC ATA TAC GGC	144
Leu Ile Phe Glu Arg Gly Glu Gly Val Tyr Leu Trp Asp Ile Tyr Gly	
35 40 45	
AGG AAG TAT ATA GAT GCC ATA TCT TCC CTC TGG TGC AAC GTC CAC GGA	192
Arg Lys Tyr Ile Asp Ala Ile Ser Ser Leu Trp Cys Asn Val His Gly	
50 55 60	
CAT AAC CAC CCT AAA CTG AAC AAC GCA GTT ATG AAA CAG CTC TGT AAG	240
His Asn His Pro Lys Leu Asn Asn Ala Val Met Lys Gln Leu Cys Lys	
65 70 75 80	
GTA GCT CAC ACA ACT ACT CTG GGA AGT TCC AAC GTT CCC GCC ATA CTC	288
Val Ala His Thr Thr Thr Leu Gly Ser Ser Asn Val Pro Ala Ile Leu	
85 90 95	
CTT GCA AAG AAG CTT GTA GAA ATT TCT CCT GAA GGA TTA AAC AAG GTC	336
Leu Ala Lys Lys Leu Val Glu Ile Ser Pro Glu Gly Leu Asn Lys Val	
100 105 110	
TTT TAC TCC GAA GAC GGT GCG GAA GCA GTA GAG ATA GCG ATA AAG ATG	384
Phe Tyr Ser Glu Asp Gly Ala Glu Ala Val Glu Ile Ala Ile Lys Met	
115 120 125	
GCT TAT CAC TAC TGG AAG AAC AAG GGA GTT AAA GGG AAA AAC GTT TTC	432
Ala Tyr His Tyr Trp Lys Asn Lys Gly Val Lys Gly Lys Asn Val Phe	
130 135 140	
ATA ACG CTT TCC GAA GCC TAC CAC GGG GAT ACT GTA GGA GCG GTT AGC	480
Ile Thr Leu Ser Glu Ala Tyr His Gly Asp Thr Val Gly Ala Val Ser	
145 150 155 160	
GTA GGG GGT ATA GAA CTC TTC CAC GGA ACT TAT AAA GAT CTC CTT TTC	528
Val Gly Gly Ile Glu Leu Phe His Gly Thr Tyr Lys Asp Leu Leu Phe	
165 170 175	

AAG ACT ATA AAA CTC CCA TCT CCT TAC CTG TAC TGC AAG GAA AAG TAC	576
Lys Thr Ile Lys Leu Pro Ser Pro Tyr Leu Tyr Cys Lys Glu Lys Tyr	
180 185 190	
GGG GAA CTC TGC CCT GAG TGC ACG GCA GAT TTA TTA AAA CAA CTG GAA	624
Gly Glu Leu Cys Pro Glu Cys Thr Ala Asp Leu Leu Lys Gln Leu Glu	
195 200 205	
GAT ATC CTG AAG TCG CGG GAA GAT ATC GTT GCG GTC ATT ATG GAA GCG	672
Asp Ile Leu Lys Ser Arg Glu Asp Ile Val Ala Val Ile Met Glu Ala	
210 215 220	
GGA ATT CAG GCA GCC GCG GGA ATG CTC CCC TTC CCT CCG GGA TTT TTG	720
Gly Ile Gln Ala Ala Glu Gly Met Leu Pro Phe Pro Gly Phe Leu	
225 230 235 240	
AAA GGC GTA AGG GAG CTT ACG AAG AAA TAC GAC ACT TTA ATG ATA GTT	768
Lys Gly Val Arg Glu Leu Thr Lys Lys Tyr Asp Thr Leu Met Ile Val	
245 250 255	
GAC GAG GTT GCC ACG GGA TTT GGC AGG ACG GGA ACG ATG TTT TAC TGT	816
Asp Glu Val Ala Thr Gly Phe Gly Arg Thr Gly Thr Met Phe Tyr Cys	
260 265 270	
GAG CAG GAA GGA GTC AGT CCG GAC TTT ATG TGT CTA GGT AAG GGT ATA	864
Glu Gln Glu Gly Val Ser Pro Asp Phe Met Cys Leu Gly Lys Gly Ile	
275 280 285	
ACC GGA GGG TAC CTC CCG CTT GCT GCG ACA CTC ACA ACG GAC GAG GTG	912
Thr Gly Gly Tyr Leu Pro Leu Ala Ala Thr Leu Thr Thr Asp Glu Val	
290 295 300	
TTC AAT GCC TTT TTA GGT GAG TTC GGG GAG GCA AAG CAC TTT TAC CAC	960
Phe Asn Ala Phe Leu Gly Glu Phe Gly Glu Ala Lys His Phe Tyr His	
305 310 315 320	
GGG CAC ACC TAC ACT GGA AAT AAC CTC GCC TGT TCC GTT GCA CTC GCA	1008
Gly His Thr Tyr Thr Gly Asn Asn Leu Ala Cys Ser Val Ala Leu Ala	
325 330 335	
AAC TTA GAA GTT TTT GAG GAA GAA AGA ACT TTA GAG AAG CTC CAA CCA	1056
Asn Leu Glu Val Phe Glu Glu Glu Arg Thr Leu Glu Lys Leu Gln Pro	
340 345 350	
AAG ATA AAG CTT TTA AAG GAA AGG CTT CAG GAG TTC TGG GAA CTC AAG	1104
Lys Ile Lys Leu Leu Lys Glu Arg Leu Gln Glu Phe Trp Glu Leu Lys	
355 360 365	
CAC GTT GGA GAT GTT AGA CAG CTA GGT TTT ATG GCT GGA ATA GAG CTG	1152
His Val Gly Asp Val Arg Gln Leu Gly Phe Met Ala Gly Ile Glu Leu	
370 375 380	
GTG AAG GAC AAA GAA AAG GGA GAA CCT TTC CCT TAC GGT GAA AGG ACG	1200
Val Lys Asp Lys Glu Lys Gly Glu Pro Phe Pro Tyr Gly Glu Arg Thr	
385 390 395 400	
GGA TTT AAG GTG GCT TAC AAG TGC AGG GAA AAA GGG GTG TTT TTG AGA	1245
Gly Phe Lys Val Ala Tyr Lys Cys Arg Glu Lys Gly Val Phe Leu Arg	
405 410 415	
CCG CTC GGA GAC GTT ATG GTA TTG ATG ATG CCT CTT GTA ATA GAG GAA	1293
Pro Leu Gly Asp Val Met Val Leu Met Met Pro Leu Val Ile Glu Glu	

420	425	430	
GAC GAA ATG AAC TAC GTT ATT GAT ACA CTT AAA TGG GCA ATT AAA GAG Asp Glu Met Asn Tyr Val Ile Asp Thr Leu Lys Trp Ala Ile Lys Glu			1341
435	440	445	
CTT GAA AAA GAG GTG TAG Leu Glu Lys Glu Val End			1359
450			
 (2) INFORMATION FOR SEQ ID NO:20:			
(i) SEQUENCE CHARACTERISTICS			
(A) LENGTH: 1032 NUCLEOTIDES			
(B) TYPE: NUCLEIC ACID			
(C) STRANDEDNESS: SINGLE			
(D) TOPOLOGY: LINEAR			
(ii) MOLECULE TYPE: GENOMIC DNA			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:			
ATG ACA TAC TTA ATG AAC AAT TAC GCA AGG TTG CCC GTA AAG TTT GTA Met Thr Tyr Leu Met Asn Asn Tyr Ala Arg Leu Pro Val Lys Phe Val			48
5	10	15	
AGG GGA AAA GGT GTT TAC CTG TAC GAT GAG GAA GGA AAG GAG TAT CTT Arg Gly Lys Gly Val Tyr Leu Tyr Asp Glu Glu Gly Lys Glu Tyr Leu			96
20	25	30	
GAC TTT GTC TCC GGT ATA GGC GTC AAC TCC CTC GGT CAC GCT TAC CCA Asp Phe Val Ser Gly Ile Gly Val Asn Ser Leu Gly His Ala Tyr Pro			144
35	40	45	
AAA CTC ACA GAA GCT CTA AAA GAA CAG GTT GAG AAA CTC CTC CAC GTT Lys Leu Thr Glu Ala Leu Lys Glu Gln Val Glu Lys Leu Leu His Val			192
50	55	60	
TCA AAT CTT TAC GAA AAC CCG TGG CAG GAA GAA CTG GCT CAC AAA CTT Ser Asn Leu Tyr Glu Asn Pro Trp Gln Glu Glu Leu Ala His Lys Leu			240
65	70	75	
GTA AAA CAC TTC TGG ACA GAA GGG AAG GTA TTT TTC GCA AAC AGC GGA Val Lys His Phe Trp Thr Glu Gly Lys Val Phe Phe Ala Asn Ser Gly			288
85	90	95	
ACG GAA AGT GTA GAG GCG GCT ATA AAG CTC GCA AGG AAG TAC TGG AGG Thr Glu Ser Val Glu Ala Ala Ile Lys Leu Ala Arg Lys Tyr Trp Arg			336
100	105	110	
GAT AAA GGA AAG AAC AAG TGG AAG TTT ATA TCC TTT GAA AAC TCT TTC Asp Lys Gly Lys Asn Lys Trp Lys Phe Ile Ser Phe Glu Asn Ser Phe			384
115	120	125	
CAC GGG AGA ACC TAC GGT AGC CTC TCC GCA ACG GGA CAG CCA AAG TTC His Gly Arg Thr Tyr Gly Ser Leu Ser Ala Thr Gly Gln Pro Lys Phe			432
130	135	140	
CAC AAA GGC TTT GAA CCT CTA GTT CCT GGA TTT TCT TAC GCA AAG CTG His Lys Gly Phe Glu Pro Leu Val Pro Gly Phe Ser Tyr Ala Lys Leu			480
145	150	155	
AAC GAT ATA GAC AGC GTT TAC AAA CTC CTA GAC GAG GAA ACC GCG GGG			528

Asn Asp Ile Asp Ser Val Tyr Lys Leu Leu Asp Glu Glu Thr Ala Gly	
165 170 175	
ATA ATT ATT GAA GTT ATA CAA GGA GAG GGC GGA GTA AAC GAG GCG AGT	576
Ile Ile Ile Glu Val Ile Gln Gly Glu Gly Gly Val Asn Glu Ala Ser	
180 185 190	
GAG GAT TTT CTA AGT AAA CTC CAG GAA ATT TGT AAA GAA AAA GAT GTG	624
Glu Asp Phe Leu Ser Lys Leu Gln Glu Ile Cys Lys Glu Lys Asp Val	
195 200 205	
CTC TTA ATT ATA GAC GAA GTG CAA ACG GGA ATA GGA AGG ACC GGG GAA	672
Leu Leu Ile Ile Asp Glu Val Gln Thr Gly Ile Gly Arg Thr Gly Glu	
210 215 220	
TTC TAC GCA TAT CAA CAC TTC AAT CTA AAA CCG GAC GTA ATT GCG CTT	720
Phe Tyr Ala Tyr Gln His Phe Asn Leu Lys Pro Asp Val Ile Ala Leu	
225 230 235 240	
GCG AAG GGA CTC GGA GGA GGT GTG CCA ATA GGT GCC ATC CTT GCA AGG	768
Ala Lys Gly Leu Gly Gly Val Pro Ile Gly Ala Ile Leu Ala Arg	
245 250 255	
GAA GAA GTG GCC CAG AGC TTT ACT CCC GGC TCC CAC GGC TCT ACC TTC	816
Glu Glu Val Ala Gln Ser Phe Thr Pro Gly Ser His Gly Ser Thr Phe	
260 265 270	
GGA GGA AAC CCC TTA GCC TGC AGG GCG GGA ACA GTG GTA GTA GAT GAA	864
Gly Gly Asn Pro Leu Ala Cys Arg Ala Gly Thr Val Val Val Asp Glu	
275 280 285	
GTT GAA AAA CTC CTG CCT CAC GTA AGG GAA GTG GGG AAT TAC TTC AAA	912
Val Glu Lys Leu Leu Pro His Val Arg Glu Val Gly Asn Tyr Phe Lys	
290 295 300	
GAA AAA CTG AAG GAA CTC GGC AAA GGA AAG GTA AAG GGA AGA GGA TTG	960
Glu Lys Leu Lys Glu Leu Gly Lys Gly Lys Val Lys Gly Arg Gly Leu	
305 310 315 320	
ATG CTC GGT CTT GAA CTT GAA AGA GAG TGT AAA GAT TAC GTT CTC AAG	1008
Met Leu Gly Leu Glu Leu Glu Arg Glu Cys Lys Asp Tyr Val Leu Lys	
325 330 335	
GCT CTT GAA AGG GAC TTC TCA TAA	1032
Ala Leu Glu Arg Asp Phe Ser End	
340	

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1197 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG CGG AAA CTG GCC GAG CGG GCG CAG AAA CTG AGC CCC TCT CCC ACC	48
Met Arg Lys Leu Ala Glu Arg Ala Gln Lys Leu Ser Pro Ser Pro Thr	
5 10 15	

CTC TCG GTG GAC ACC AAG GCC AAG GAG CTT TTG CGG CAG GGG GAA AGG Leu Ser Val Asp Thr Lys Ala Lys Glu Leu Leu Arg Gln Gly Glu Arg 20 25 30	96
GTC ATC AAT TTC GGG GCG GGG GAG CCG GAC TTC GAT ACA CCG GAA CAC Val Ile Asn Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Glu His 35 40 45	144
ATC AAG GAA GCG GCG AAG CGA GCT TTA GAT CAG GGC TTC ACC AAG TAC Ile Lys Glu Ala Ala Lys Arg Ala Leu Asp Gln Gly Phe Thr Lys Tyr 50 55 60	192
ACG CCG GTG GCT GGG ATC TTA CCT CTT CGG GAG GCC ATA TGC GAG AAG Thr Pro Val Ala Gly Ile Leu Pro Leu Arg Glu Ala Ile Cys Glu Lys 65 70 75 80	240
CTT TAC CGC GAC AAT CAA CTG GAA TAC AGC CCG AAT GAG ATC GTG GTC Leu Tyr Arg Asp Asn Gln Leu Glu Tyr Ser Pro Asn Glu Ile Val Val 85 90 95	288
TCC TGT GGC GCC AAG CAT TCT ATT TTC AAC GCT CTG CAG GTC CTC CTG Ser Cys Gly Ala Lys His Ser Ile Phe Asn Ala Leu Gln Val Leu Leu 100 105 110	336
GAC CCG GGG GAC GAG GTG ATA ATC CCC GTC CCC TAC TGG ACT TCC TAT Asp Pro Gly Asp Glu Val Ile Ile Pro Val Pro Tyr Trp Thr Ser Tyr 115 120 125	384
CCG GAG CAG GTG AAG CTG GCG GGA GGG GTG CCG GTT TTC GTC CCC ACC Pro Glu Gln Val Lys Leu Ala Gly Gly Val Pro Val Phe Val Pro Thr 130 135 140	432
TCT CCC GAG AAC GAC TTC AAG CTC AGG CCG GAA GAT CTA CGT GCG GCT Ser Pro Glu Asn Asp Phe Lys Leu Arg Pro Glu Asp Leu Arg Ala Ala 145 150 155 160	480
GTA ACC CCG CGC ACC CGC CTT TTG ATC CTC AAT TCC CCG GCC AAC CCC Val Thr Pro Arg Thr Arg Leu Leu Ile Leu Asn Ser Pro Ala Asn Pro 165 170 175	528
ACA GGC ACC GTT TAC CGC CGG GAG GAA CTT ATC GGC TTA GCG GAG GTA Thr Gly Thr Val Tyr Arg Arg Glu Glu Leu Ile Gly Leu Ala Glu Val 180 185 190	576
GCC CTG GAG GCC GAC CTA TGG ATC TTG TCG GAC GAG ATC TAC GAA AAG Ala Leu Glu Ala Asp Leu Trp Ile Leu Ser Asp Glu Ile Tyr Glu Lys 195 200 205	624
CTG ATC TAC GAC GGG ATG GAG CAC GTG AGC ATA GCC GCG CTC GAC CCG Leu Ile Tyr Asp Gly Met Glu His Val Ser Ile Ala Ala Leu Asp Pro 210 215 220	672
GAG GTC AAA AAG CGC ACG ATT GTG GTA AAC GGT GTT TCC AAG GCT TAC Glu Val Lys Lys Arg Thr Ile Val Val Asn Gly Val Ser Lys Ala Tyr 225 230 235 240	720
GCC ATG ACC GGT TGG CGC ATA GGT TAT GCT GCC GCT CCC CGG CCG ATA Ala Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Ala Pro Arg Pro Ile 245 250 255	768
GCC CAG GCC ATG ACC AAC CTC CAA AGC CAC AGT ACC TCT AAC CCC ACT Ala Gln Ala Met Thr Asn Leu Gln Ser His Ser Thr Ser Asn Pro Thr	816

260	265	270	
TCC GTA GCC CAG GCG GCG GCG CTG GCC GCT CTG AAG GGG CCA CAA GAG Ser Val Ala Gln Ala Ala Ala Leu Ala Ala Leu Lys Gly Pro Gln Glu 275 280 285			864
CCG GTG GAG AAC ATG CGC CGG GCT TTT CAA AAG CGG CGG GAT TTC ATC Pro Val Glu Asn Met Arg Arg Ala Phe Gln Lys Arg Arg Asp Phe Ile 290 295 300			912
TGG CAG TAC CTA AAC TCC TTA CCC GGA GTG CGC TGC CCC AAA CCT TTA Trp Gln Tyr Leu Asn Ser Leu Pro Gly Val Arg Cys Pro Lys Pro Leu 305 310 315 320			960
GGG GCC TTT TAC GTC TTT CCA GAA GTT GAG CGG GCT TTT GGG CCG CCG Gly Ala Phe Tyr Val Phe Pro Glu Val Glu Arg Ala Phe Gly Pro Pro 325 330 335			1008
TCT AAA AGG ACG GGA AAT ACT ACC GCT AGC GAC CTG GCC CTT TTC CTC Ser Lys Arg Thr Gly Asn Thr Thr Ala Ser Asp Leu Ala Leu Phe Leu 340 345 350			1056
CTG GAA GAG ATA AAA GTG GCC ACC GTG GCT GGG GCT GCC TTT GGG GAC Leu Glu Glu Ile Lys Val Ala Thr Val Ala Gly Ala Ala Phe Gly Asp 355 360 365			1104
GAT CGC TAC CTG CGC TTT TCC TAC GCC CTG CGG CTG GAA GAT ATC GAA Asp Arg Tyr Leu Arg Phe Ser Tyr Ala Leu Arg Leu Glu Asp Ile Glu 370 375 380			1152
GAG GGG ATG CAA CGG TTT AAA GAA TTG ATC GAA GCG GCA CTT TAA Glu Gly Met Gln Arg Phe Lys Glu Leu Ile Glu Ala Ala Leu End 385 390 395			1197

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1779 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG TGC GGG ATA GTC GGA TAC GTA GGG AGG GAT TTA GCC CTT CCT ATA Met Cys Gly Ile Val Gly Tyr Val Gly Arg Asp Leu Ala Leu Pro Ile 5 10 15	48
GTC CTC GGA GCT CTT GAG AGA CTC GAA TAC AGG GGT TAC GAC TCC GCG Val Leu Gly Ala Leu Glu Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala 20 25 30	96
GGA GTT GCC CTT ATA GAA GAC GGG AAA CTC ATA GTT GAA AAG AAG AAG Gly Val Ala Leu Ile Glu Asp Gly Lys Leu Ile Val Glu Lys Lys Lys 35 40 45	144
GGA AAG ATA AGG GAA CTC GTT AAA GCG CTA TGG GGA AAG GAT TAC AAG Gly Lys Ile Arg Glu Leu Val Lys Ala Leu Trp Gly Lys Asp Tyr Lys 50 55 60	192

GCT AAA ACG GGT ATA GGT CAC ACA CGC TGG GCA ACC CAC GGA AAG CCC Ala Lys Thr Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Lys Pro 65 70 75 80	240
ACG GAC GAG AAC GCC CAC CCC CAC ACC GAC GAA AAA GGT GAG TTT GCA Thr Asp Glu Asn Ala His Pro His Thr Asp Glu Lys Gly Glu Phe Ala 85 90 95	288
GTA GTT CAC AAC GGG ATA ATA GAA AAC TAC TTA GAA CTA AAA GAG GAA Val Val His Asn Gly Ile Ile Glu Asn Tyr Leu Glu Leu Lys Glu Glu 100 105 110	336
CTA AAG AAG GAA GGT GTA AAG TTC AGG TCC GAA ACA GAC ACA GAA GTT Leu Lys Lys Glu Gly Val Lys Phe Arg Ser Glu Thr Asp Thr Glu Val 115 120 125	384
ATA GCC CAC CTC ATA GCG AAG AAC TAC AGG GGG GAC TTA CTG GAG GCC Ile Ala His Leu Ile Ala Lys Asn Tyr Arg Gly Asp Leu Leu Glu Ala 130 135 140	432
GTT TTA AAA ACC GTA AAG AAA TTA AAG GGT GCT TTT GCC TTT GCG GTT Val Leu Lys Thr Val Lys Lys Leu Lys Gly Ala Phe Ala Phe Ala Val 145 150 155 160	480
ATA ACG GTT CAC GAA CCA AAC AGA CTA ATA GGA GTG AAG CAG GGG AGT Ile Thr Val His Glu Pro Asn Arg Leu Ile Gly Val Lys Gln Gly Ser 165 170 175	528
CCT TTA ATC GTC GGA CTC GGA GAA GGA GAA AAC TTC CTC GCT TCA GAT Pro Leu Ile Val Gly Leu Gly Glu Gly Glu Asn Phe Leu Ala Ser Asp 180 185 190	576
ATT CCC GCA ATA CTT CCT TAC ACG AAA AAG ATT ATT GTT CTT GAT GAC Ile Pro Ala Ile Leu Pro Tyr Thr Lys Lys Ile Ile Val Leu Asp Asp 195 200 205	624
GGG GAA ATA GCG GAC CTG ACT CCC GAC ACT GTG AAC ATT TAC AAC TTT Gly Glu Ile Ala Asp Leu Thr Pro Asp Thr Val Asn Ile Tyr Asn Phe 210 215 220	672
GAG GGA GAG CCC GTT TCA AAG GAA GTA ATG ATT ACG CCC TGG GAT CTT Glu Gly Glu Pro Val Ser Lys Glu Val Met Ile Thr Pro Trp Asp Leu 225 230 235 240	720
GTT TCT GCG GAA AAG GGT GGT TTT AAA CAC TTC ATG CTA AAA GAG ATA Val Ser Ala Glu Lys Gly Gly Phe Lys His Phe Met Leu Lys Glu Ile 245 250 255	768
TAC GAA CAG CCC AAA GCC ATA AAC GAC ACA CTC AAG GGT TTC CTC TCA Tyr Glu Gln Pro Lys Ala Ile Asn Asp Thr Leu Lys Gly Phe Leu Ser 260 265 270	816
ACC GAA GAC GCA ATA CCC TTT AAG TTA AAA GAC TTC AGA AGG GTT TTA Thr Glu Asp Ala Ile Pro Phe Lys Leu Lys Asp Phe Arg Arg Val Leu 275 280 285	864
ATA ATA GCG TGC GGG ACC TCT TAC CAC GCG GGC TTC GTC GGA AAG TAC Ile Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Phe Val Gly Lys Tyr 290 295 300	912
TGG ATA GAG AGA TTT GCA GGT GTT CCC ACA GAG GTA ATT TAC GCT TCG Trp Ile Glu Arg Phe Ala Gly Val Pro Thr Glu Val Ile Tyr Ala Ser	960

305	310	315	320	
GAA TTC AGG TAT GCG GAC GTT CCC GTT TCG GAC AAG GAT ATC GTT ATC Glu Phe Arg Tyr Ala Asp Val Pro Val Ser Asp Lys Asp Ile Val Ile	325	330	335	1008
GGA ATT TCC CAG TCA GGA GAG ACC GCT GAC ACA AAG TTT GCC CTT CAG Gly Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Lys Phe Ala Leu Gln	340	345	350	1056
TCC GCA AAG GAA AAG GGA GCC TTT ACC GTG GGA CTC GTA AAC GTA GTG Ser Ala Lys Glu Lys Gly Ala Phe Thr Val Gly Leu Val Asn Val Val	355	360	365	1104
GGA AGT GCC ATA GAC AGG GAG TCG GAC TTT TCC CTT CAC ACA CAT GCG Gly Ser Ala Ile Asp Arg Glu Ser Asp Phe Ser Leu His Thr His Ala	370	375	380	1152
GGA CCC GAA ATA GGC GTG GCG GCT ACA AAG ACC TTC ACC GCA CAG TTC Gly Pro Glu Ile Gly Val Ala Ala Thr Lys Thr Phe Thr Ala Gln Phe	385	390	395	1200
ACC GCA CTC TAC GCC CTT TCG GTA AGG GAA AGT GAG GAG AGG GAA AAT Thr Ala Leu Tyr Ala Leu Ser Val Arg Glu Ser Glu Glu Arg Glu Asn	405	410	415	1248
CTA ATA AGA CTC CTT GAA AAG GTT CCA TCA CTC GTT GAA CAA ACA CTG Leu Ile Arg Leu Leu Glu Lys Val Pro Ser Leu Val Glu Gln Thr Leu	420	425	430	1296
AAC ACC GCA GAA GAA GTG GAG AAG GTA GCG GAA AAG TAC ATG AAA AAG Asn Thr Ala Glu Glu Val Glu Lys Val Ala Glu Lys Tyr Met Lys Lys	435	440	445	1344
AAA AAC ATG CTT TAC CTC GGA AGG TAC TTA AAT TAC CCC ATA GCG CTG Lys Asn Met Leu Tyr Leu Gly Arg Tyr Leu Asn Tyr Pro Ile Ala Leu	450	455	460	1392
GAG GGA GCT CTT AAA CTT AAA GAA ATT TCT TAC ATA CAC GCG GAA GGT Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Gly	465	470	475	1440
TAT CCC GCA GGG GAG ATG AAG CAC GGT CCC ATA GCC CTC ATA GAC GAA Tyr Pro Ala Gly Glu Met Lys His Gly Pro Ile Ala Leu Ile Asp Glu	485	490	495	1488
AAC ATG CCG GTT GTG GTA ATC GCA CCG AAA GAC AGG GTT TAC GAG AAG Asn Met Pro Val Val Val Ile Ala Pro Lys Asp Arg Val Tyr Glu Lys	500	505	510	1536
ATA CTC TCA AAC GTA GAA GAG GTT CTC GCA AGA AAG GGA AGG GTT ATT Ile Leu Ser Asn Val Glu Glu Val Leu Ala Arg Lys Gly Arg Val Ile	515	520	525	1584
TCT GTA GGC TTT AAA GGA GAC GAA ACT CTC AAA AGC AAA TCC GAG AGC Ser Val Gly Phe Lys Gly Asp Glu Thr Leu Lys Ser Lys Ser Glu Ser	530	535	540	1632
GTT ATG GAA ATC CCG AAG GCA GAA GAA CCG ATA ACT CCT TTC TTG ACG Val Met Glu Ile Pro Lys Ala Glu Glu Pro Ile Thr Pro Phe Leu Thr	545	550	555	1680
GTA ATA CCC CTG CAA CTC TTT GCC TAC TTT ATA GCG AGC AAA CTG GGA Val Ile Pro Leu Gln Leu Phe Ala Tyr Phe Ile Ala Ser Lys Leu Gly				1728

565	570	575	580
CTG GAT GTG GAT CAG CCG AGA AAT CTC GCC AAA ACG GTC ACG GTG GAA			1776
Leu Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Thr Val Thr Val Glu			
580	585	590	

TAA 1779
End

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1065 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG ATA CCC CAG AGG ATT AAG GAA CTT GAA GCT TAC AAG ACG GAG GTC	48
Met Ile Pro Gln Arg Ile Lys Glu Leu Glu Ala Tyr Lys Thr Glu Val	
5 10 15	
ACT CCC GCC TCC GTC AGG CTT TCC TCT AAC GAA TTC CCC TAC GAC TTT	96
Thr Pro Ala Ser Val Arg Leu Ser Ser Asn Glu Phe Pro Tyr Asp Phe	
20 25 30	
CCC GAG GAG ATA AAA CAA AGG GCC TTA GAA GAA TTA AAA AAG GTT CCC	144
Pro Glu Glu Ile Lys Gln Arg Ala Leu Glu Glu Leu Lys Lys Val Pro	
35 40 45	
TTG AAC AAA TAC CCA GAC CCC GAA GCG AAA GAG TTA AAA GCG GTT CTT	192
Leu Asn Lys Tyr Pro Asp Pro Glu Ala Lys Glu Leu Lys Ala Val Leu	
50 55 60	
GCG GAT TTT TTC GGC GTT AAG GAA GAA AAT TTA GTT CTC GGT AAC GGT	240
Ala Asp Phe Phe Gly Val Lys Glu Glu Asn Leu Val Leu Gly Asn Gly	
65 70 75 80	
TCG GAC GAA CTC ATA TAC TAC CTC TCA ATA GCT ATA GGT GAA CTT TAC	288
Ser Asp Glu Leu Ile Tyr Tyr Leu Ser Ile Ala Ile Gly Glu Leu Tyr	
85 90 95	
ATA CCC GTT TAC ATA CCT GTT CCC ACC TTT CCC ATG TAC GAG ATA AGT	336
Ile Pro Val Tyr Ile Pro Val Pro Thr Phe Pro Met Tyr Glu Ile Ser	
100 105 110	
GCG AAA GTT CTC GGA AGA CCC CTC GTA AAG GTT CAA CTG GAC GAA AAC	384
Ala Lys Val Leu Gly Arg Pro Leu Val Lys Val Gln Leu Asp Glu Asn	
115 120 125	
TTT GAT ATA GAC TTA GAA AGA AGT ATT GAA TTA ATA GAG AAA GAA AAA	432
Phe Asp Ile Asp Leu Glu Arg Ser Ile Glu Leu Ile Glu Lys Glu Lys	
130 135 140	
CCC GTT CTC GGG TAC TTT GCT TAC CCA AAC AAC CCC ACG GGA AAC CTC	480
Pro Val Leu Gly Tyr Phe Ala Tyr Pro Asn Asn Pro Thr Gly Asn Leu	
145 150 155 160	
TTT TCC AGG GGA AAG ATT GAG GAG ATA AGA AAC AGG GGT GTT TTC TGT	528
Phe Ser Arg Gly Lys Ile Glu Glu Ile Arg Asn Arg Gly Val Phe Cys	

165	170	175	
GTA ATA GAC GAA GCC TAC TAT CAT TAC TCC GGA GAA ACC TTT CTG GAA Val Ile Asp Glu Ala Tyr Tyr His Tyr Ser Gly Glu Thr Phe Leu Glu 180 185 190			576
GAC GCG CTC AAA AGG GAA GAT ACG GTA GTT TTG AGG ACA CTT TCA AAA Asp Ala Leu Lys Arg Glu Asp Thr Val Val Leu Arg Thr Leu Ser Lys 195 200 205			624
ATC GGT ATG GCG AGT TTA AGG GTA GGG ATT TTA ATA GGG AAG GGG GAA Ile Gly Met Ala Ser Leu Arg Val Gly Ile Leu Ile Gly Lys Gly Glu 210 215 220			672
ATC GTC TCA GAA ATT AAC AAG GTG AGA CTC CCC TTC AAC GTG ACC TAC Ile Val Ser Glu Ile Asn Lys Val Arg Leu Pro Phe Asn Val Thr Tyr 225 230 235 240			720
CCC TCT CAG GTG ATG GCA AAA GTT CTC CTC ACG GAG GGA AGA GAA TTC Pro Ser Gln Val Met Ala Lys Val Leu Leu Thr Glu Gly Arg Glu Phe 245 250 255			768
CTA ATG GAA AAG ATA CAG GAG GTT GTA ACA GAG CGA GAA AGG ATG TAC Leu Met Glu Lys Ile Gln Glu Val Val Thr Glu Arg Glu Arg Met Tyr 260 265 270			816
GAC GAA ATG AAG AAA ATA GAA GGA GTT GAG GTT TTT CCG AGT AAG GCT Asp Glu Met Lys Lys Ile Glu Gly Val Glu Val Phe Pro Ser Lys Ala 275 280 285			864
AAC TTC TTG CTT TTC AGA ACG CCT TAC CCC GCC CAC GAG GTT TAT CAG Asn Phe Leu Leu Phe Arg Thr Pro Tyr Pro Ala His Glu Val Tyr Gln 290 295 300			912
GAG CTA CTG AAA AGG GAT GTC CTC GTC AGG AAC GTA TCT TAC ATG GAA Glu Leu Leu Lys Arg Asp Val Leu Val Arg Asn Val Ser Tyr Met Glu 305 310 315 320			960
GGA CTC CAA AAG TGC CTC AGG GTA AGC GTA GGG AAA CCG GAA GAA AAC Gly Leu Gln Lys Cys Leu Arg Val Ser Val Gly Lys Pro Glu Glu Asn 325 330 335			1008
AAC AAG TTT CTG GAA GCA CTG GAG GAG AGT ATA AAA TCC CTT TCA AGC Asn Lys Phe Leu Glu Ala Leu Glu Glu Ser Ile Lys Ser Leu Ser Ser 340 345 350			1056
TCT CTT TAA Ser Leu End			1065

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 912 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG AAG CCG TAC GCT AAA TAT ATC TGG CTT GAC GGC AGA ATA CTT AAG 48

Met	Lys	Pro	Tyr	Ala	Lys	Tyr	Ile	Trp	Leu	Asp	Gly	Arg	Ile	Leu	Lys	
				5					10					15		
TGG	GAA	GAC	GCG	AAA	ATA	CAC	GTG	TTG	ACT	CAC	GCG	CTT	CAC	TAC	GGA	96
Trp	Glu	Asp	Ala	Lys	Ile	His	Val	Leu	Thr	His	Ala	Leu	His	Tyr	Gly	
			20					25					30			
ACC	TCT	ATA	TTC	GAG	GGA	ATA	AGA	GGG	TAT	TGG	AAC	GGC	GAT	AAT	TTG	144
Thr	Ser	Ile	Phe	Glu	Gly	Ile	Arg	Gly	Tyr	Trp	Asn	Gly	Asp	Asn	Leu	
			35				40					45				
CTC	GTC	TTT	AGG	TTA	GAA	GAA	CAC	ATC	GAC	CGC	ATG	TAC	AGA	TCG	GCT	192
Leu	Val	Phe	Arg	Leu	Glu	Glu	His	Ile	Asp	Arg	Met	Tyr	Arg	Ser	Ala	
			50				55				60					
AAG	ATA	CTA	GGC	ATA	AAT	ATT	CCG	TAT	ACA	AGA	GAG	GAA	GTC	CGC	CAA	240
Lys	Ile	Leu	Gly	Ile	Asn	Ile	Pro	Tyr	Thr	Arg	Glu	Glu	Val	Arg	Gln	
			65			70				75					80	
GCT	GTA	CTA	GAG	ACC	ATA	AAG	GCT	AAT	AAC	TTC	CGA	GAG	GAT	GTC	TAC	288
Ala	Val	Leu	Glu	Thr	Ile	Lys	Ala	Asn	Asn	Phe	Arg	Glu	Asp	Val	Tyr	
				85					90					95		
ATA	AGA	CCT	GTG	GCG	TTT	GTC	GCC	TCG	CAG	ACG	GTG	ACG	CTT	GAC	ATA	336
Ile	Arg	Pro	Val	Ala	Phe	Val	Ala	Ser	Gln	Thr	Val	Thr	Leu	Asp	Ile	
				100				105					110			
AGA	AAT	TTG	GAA	GTC	TCC	CTC	GCG	GTT	ATT	GTA	TTC	CCA	TTT	GGC	AAA	384
Arg	Asn	Leu	Glu	Val	Ser	Leu	Ala	Val	Ile	Val	Phe	Pro	Phe	Gly	Lys	
			115				120					125				
TAC	CTC	TCG	CCC	AAC	GGC	ATT	AAG	GCA	ACG	ATT	GTA	AGC	TGG	CGT	AGA	432
Tyr	Leu	Ser	Pro	Asn	Gly	Ile	Lys	Ala	Thr	Ile	Val	Ser	Trp	Arg	Arg	
			130			135					140					
GTA	CAT	AAT	ACA	ATG	CTC	CCT	GTG	ATG	GCA	AAA	ATC	GGC	GGT	ATA	TAT	480
Val	His	Asn	Thr	Met	Leu	Pro	Val	Met	Ala	Lys	Ile	Gly	Gly	Ile	Tyr	
					150				155					160		
GTA	AAC	TCT	GTA	CTT	GCG	CTT	GTA	GAG	GCT	AGA	AGC	AGG	GGA	TTT	GAC	528
Val	Asn	Ser	Val	Leu	Ala	Leu	Val	Glu	Ala	Arg	Ser	Arg	Gly	Phe	Asp	
				165				170						175		
GAG	GCT	TTA	TTA	ATG	GAC	GTT	AAC	GGT	TAT	GTT	GTT	GAG	GGT	TCT	GGA	576
Glu	Ala	Leu	Leu	Met	Asp	Val	Asn	Gly	Tyr	Val	Val	Glu	Gly	Ser	Gly	
			180					185					190			
GAG	AAT	ATT	TTC	ATT	GTC	AGA	GGT	GGA	AGG	CTT	TTC	ACG	CCG	CCA	GTA	624
Glu	Asn	Ile	Phe	Ile	Val	Arg	Gly	Gly	Arg	Leu	Phe	Thr	Pro	Pro	Val	
			195				200					205				
CAC	GAA	TCT	ATC	CTC	GAG	GGA	ATT	ACG	AGG	GAT	ACG	GTA	ATA	AAG	CTC	672
His	Glu	Ser	Ile	Leu	Glu	Gly	Ile	Thr	Arg	Asp	Thr	Val	Ile	Lys	Leu	
			210			215					220					
AGC	GGG	GAT	GTG	GGA	CTT	CGG	GTG	GAG	GAA	AAG	CCT	ATT	ACG	AGG	GAG	720
Ser	Gly	Asp	Val	Gly	Leu	Arg	Val	Glu	Glu	Lys	Pro	Ile	Thr	Arg	Glu	
			225		230					235					240	
GAG	GTG	TAT	ACA	GCC	GAC	GAG	GTG	TTT	TTA	GTA	GGA	ACC	GCC	GCA	GAG	768
Glu	Val	Tyr	Thr	Ala	Asp	Glu	Val	Phe	Leu	Val	Gly	Thr	Ala	Ala	Glu	
				245					250					255		

ATA ACG CCA GTG GTG GAG GTT GAC GGC AGA ACA ATC GGC ACA GGC AAG	816
Ile Thr Pro Val Val Glu Val Asp Gly Arg Thr Ile Gly Thr Gly Lys	
260 265 270	
CCG GGC CCC ATT ACG ACA AAA ATA GCT GAG CTG TAC TCA AAC GTC GTG	864
Pro Gly Pro Ile Thr Thr Lys Ile Ala Glu Leu Tyr Ser Asn Val Val	
275 280 285	
AGA GGC AAA GTA GAG AAA TAC TTA AAT TGG ATC ACT CCT GTG TAT TAG	912
Arg Gly Lys Val Glu Lys Tyr Leu Asn Trp Ile Thr Pro Val Tyr End	
290 295 300	

- (2) INFORMATION FOR SEQ ID NO:25:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 414 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ile Glu Asp Pro Met Asp Trp Ala Phe Pro Arg Ile Lys Arg Leu	
5 10 15	
Pro Gln Tyr Val Phe Ser Leu Val Asn Glu Leu Lys Tyr Lys Leu Arg	
20 25 30	
Arg Glu Gly Glu Asp Val Val Asp Leu Gly Met Gly Asn Pro Asn Met	
35 40 45	
Pro Pro Ala Lys His Ile Ile Asp Lys Leu Cys Glu Val Ala Gln Lys	
50 55 60	
Pro Asn Val His Gly Tyr Ser Ala Ser Arg Gly Ile Pro Arg Leu Arg	
65 70 75 80	
Lys Ala Ile Cys Asn Phe Tyr Glu Glu Arg Tyr Gly Val Lys Leu Asp	
85 90 95	
Pro Glu Arg Glu Ala Ile Leu Thr Ile Gly Ala Lys Glu Gly Tyr Ser	
100 105 110	
His Leu Met Leu Ala Met Ile Ser Pro Gly Asp Thr Val Ile Val Pro	
115 120 125	
Asn Pro Thr Tyr Pro Ile His Tyr Tyr Ala Pro Ile Ile Ala Gly Gly	
130 135 140	
Glu Val His Ser Ile Pro Leu Asn Phe Ser Asp Asp Gln Asp His Gln	
145 150 155 160	
Glu Glu Phe Leu Arg Arg Leu Tyr Glu Ile Val Lys Thr Ala Met Pro	
165 170 175	
Lys Pro Lys Ala Val Val Ile Ser Phe Pro His Asn Pro Thr Thr Ile	
180 185 190	
Thr Val Glu Lys Asp Phe Phe Lys Glu Ile Val Lys Phe Ala Lys Glu	
195 200 205	

His Gly Leu Trp Ile Ile His Asp Phe Ala Tyr Ala Asp Ile Ala Phe
 210 215 220
 Asp Gly Tyr Lys Pro Pro Ser Ile Leu Glu Ile Glu Gly Ala Lys Asp
 225 230 235 240
 Val Ala Val Glu Leu Tyr Ser Met Ser Lys Gly Phe Ser Met Ala Gly
 245 250 255
 Trp Arg Val Ala Phe Val Val Gly Asn Glu Ile Leu Ile Lys Asn Leu
 260 265 270
 Ala His Leu Lys Ser Tyr Leu Asp Tyr Gly Ile Phe Thr Pro Ile Gln
 275 280 285
 Val Ala Ser Ile Ile Ala Leu Glu Ser Pro Tyr Glu Ile Val Glu Lys
 290 295 300
 Thr Ala Lys Val Tyr Gln Lys Arg Arg Asp Val Leu Val Glu Gly Leu
 305 310 315 320
 Asn Arg Leu Gly Trp Lys Val Lys Lys Pro Lys Ala Thr Met Phe Val
 325 330 335
 Trp Ala Lys Ile Pro Glu Trp Ile Asn Met Asn Ser Leu Asp Phe Ser
 340 345 350
 Leu Phe Leu Leu Lys Glu Ala Lys Val Ala Val Ser Pro Gly Val Gly
 355 360 365
 Phe Gly Gln Tyr Gly Glu Gly Tyr Val Arg Phe Ala Leu Val Glu Asn
 370 375 380
 Glu His Arg Ile Arg Gln Ala Ile Arg Gly Ile Arg Lys Ala Phe Arg
 385 390 395 400
 Lys Leu Gln Lys Glu Arg Lys Leu Glu Pro Glu Arg Ser Ala End
 405 410 414

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 373 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asp Arg Leu Glu Lys Val Ser Pro Phe Ile Val Met Asp Ile Leu
 5 10 15
 Ala Gln Ala Gln Lys Tyr Glu Asp Val Val His Met Glu Ile Gly Glu
 20 25 30
 Pro Asp Leu Glu Pro Ser Pro Lys Val Met Glu Ala Leu Glu Arg Ala
 35 40 45
 Val Lys Glu Lys Thr Phe Phe Tyr Thr Pro Ala Leu Gly Leu Trp Glu
 50 55 60
 Leu Arg Glu Arg Ile Ser Glu Phe Tyr Arg Lys Lys Tyr Ser Val Glu

65		70		75		80
Val Ser Pro Glu Arg Val Ile Val Thr Thr Gly Thr Ser Gly Ala Phe						
	85		90			95
Leu Val Ala Tyr Ala Val Thr Leu Asn Ala Gly Glu Lys Ile Ile Leu						
	100		105			110
Pro Asp Pro Ser Tyr Pro Cys Tyr Lys Asn Phe Ala Tyr Leu Leu Asp						
	115		120			125
Ala Gln Pro Val Phe Val Asn Val Asp Lys Glu Thr Asn Tyr Glu Val						
	130		135			140
Arg Lys Glu Met Ile Glu Asp Ile Asp Ala Lys Ala Leu His Ile Ser						
	145		150		155	160
Ser Pro Gln Asn Pro Thr Gly Thr Leu Tyr Ser Pro Glu Thr Leu Lys						
	165		170			175
Glu Leu Ala Glu Tyr Cys Glu Glu Lys Gly Met Tyr Phe Ile Ser Asp						
	180		185			190
Glu Ile Tyr His Gly Leu Val Tyr Glu Gly Arg Glu His Thr Ala Leu						
	195		200			205
Glu Phe Ser Asp Arg Ala Ile Val Ile Asn Gly Phe Ser Lys Tyr Phe						
	210		215			220
Cys Met Pro Gly Phe Arg Ile Gly Trp Met Ile Val Pro Glu Glu Leu						
	225		230		235	240
Val Arg Lys Ala Glu Ile Val Ile Gln Asn Val Phe Ile Ser Ala Pro						
	245		250			255
Thr Leu Ser Gln Tyr Ala Ala Leu Glu Ala Phe Asp Tyr Glu Tyr Leu						
	260		265			270
Glu Lys Val Arg Lys Thr Phe Glu Glu Arg Arg Asn Phe Leu Tyr Gly						
	275		280			285
Glu Leu Lys Lys Leu Phe Lys Ile Asp Ala Lys Pro Gln Gly Ala Phe						
	290		295			300
Tyr Val Trp Ala Asn Ile Ser Asp Tyr Ser Thr Asp Ser Tyr Glu Phe						
	305		310		315	320
Ala Leu Lys Leu Leu Arg Glu Ala Arg Val Ala Val Thr Pro Gly Val						
	325		330			335
Asp Phe Gly Lys Asn Lys Thr Lys Glu Tyr Ile Arg Phe Ala Tyr Thr						
	340		345			350
Arg Lys Ile Glu Glu Leu Lys Glu Gly Val Glu Arg Ile Lys Lys Phe						
	355		360			365
Leu Glu Lys Leu Ser						
	370					

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 453 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Trp Glu Leu Asp Pro Lys Thr Leu Glu Lys Trp Asp Lys Glu Tyr
5 10 15
Phe Trp His Pro Phe Thr Gln Met Lys Val Tyr Arg Glu Glu Asn
20 25 30
Leu Ile Phe Glu Arg Gly Glu Gly Val Tyr Leu Trp Asp Ile Tyr Gly
35 40 45
Arg Lys Tyr Ile Asp Ala Ile Ser Ser Leu Trp Cys Asn Val His Gly
50 55 60
His Asn His Pro Lys Leu Asn Asn Ala Val Met Lys Gln Leu Cys Lys
65 70 75 80
Val Ala His Thr Thr Thr Leu Gly Ser Ser Asn Val Pro Ala Ile Leu
85 90 95
Leu Ala Lys Lys Leu Val Glu Ile Ser Pro Glu Gly Leu Asn Lys Val
100 105 110
Phe Tyr Ser Glu Asp Gly Ala Glu Ala Val Glu Ile Ala Ile Lys Met
115 120 125
Ala Tyr His Tyr Trp Lys Asn Lys Gly Val Lys Gly Lys Asn Val Phe
130 135 140
Ile Thr Leu Ser Glu Ala Tyr His Gly Asp Thr Val Gly Ala Val Ser
145 150 155 160
Val Gly Gly Ile Glu Leu Phe His Gly Thr Tyr Lys Asp Leu Leu Phe
165 170 175
Lys Thr Ile Lys Leu Pro Ser Pro Tyr Leu Tyr Cys Lys Glu Lys Tyr
180 185 190
Gly Glu Leu Cys Pro Glu Cys Thr Ala Asp Leu Leu Lys Gln Leu Glu
195 200 205
Asp Ile Leu Lys Ser Arg Glu Asp Ile Val Ala Val Ile Met Glu Ala
210 215 220
Gly Ile Gln Ala Ala Ala Gly Met Leu Pro Phe Pro Pro Gly Phe Leu
225 230 235 240
Lys Gly Val Arg Glu Leu Thr Lys Lys Tyr Asp Thr Leu Met Ile Val
245 250 255
Asp Glu Val Ala Thr Gly Phe Gly Arg Thr Gly Thr Met Phe Tyr Cys
260 265 270

Glu Gln Glu Gly Val Ser Pro Asp Phe Met Cys Leu Gly Lys Gly Ile
275 280 285

Thr Gly Gly Tyr Leu Pro Leu Ala Ala Thr Leu Thr Thr Asp Glu Val
290 295 300

Phe Asn Ala Phe Leu Gly Glu Phe Gly Glu Ala Lys His Phe Tyr His
305 310 315 320

Gly His Thr Tyr Thr Gly Asn Asn Leu Ala Cys Ser Val Ala Leu Ala
325 330 335

Asn Leu Glu Val Phe Glu Glu Glu Arg Thr Leu Glu Lys Leu Gln Pro
340 345 350

Lys Ile Lys Leu Leu Lys Glu Arg Leu Gln Glu Phe Trp Glu Leu Lys
355 360 365

His Val Gly Asp Val Arg Gln Leu Gly Phe Met Ala Gly Ile Glu Leu
370 375 380

Val Lys Asp Lys Glu Lys Gly Glu Pro Phe Pro Tyr Gly Glu Arg Thr
385 390 395 400

Gly Phe Lys Val Ala Tyr Lys Cys Arg Glu Lys Gly Val Phe Leu Arg
405 410 415

Pro Leu Gly Asp Val Met Val Leu Met Met Pro Leu Val Ile Glu Glu
420 425 430

Asp Glu Met Asn Tyr Val Ile Asp Thr Leu Lys Trp Ala Ile Lys Glu
435 440 445

Leu Glu Lys Glu Val
450

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 343 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Thr Tyr Leu Met Asn Asn Tyr Ala Arg Leu Pro Val Lys Phe Val
5 10 15

Arg Gly Lys Gly Val Tyr Leu Tyr Asp Glu Glu Gly Lys Glu Tyr Leu
20 25 30

Asp Phe Val Ser Gly Ile Gly Val Asn Ser Leu Gly His Ala Tyr Pro
35 40 45

Lys Leu Thr Glu Ala Leu Lys Glu Gln Val Glu Lys Leu Leu His Val
50 55 60

Ser Asn Leu Tyr Glu Asn Pro Trp Gln Glu Glu Leu Ala His Lys Leu
65 70 75 80

Val Lys His Phe Trp Thr Glu Gly Lys Val Phe Phe Ala Asn Ser Gly
 85 90 95
 Thr Glu Ser Val Glu Ala Ala Ile Lys Leu Ala Arg Lys Tyr Trp Arg
 100 105 110
 Asp Lys Gly Lys Asn Lys Trp Lys Phe Ile Ser Phe Glu Asn Ser Phe
 115 120 125
 His Gly Arg Thr Tyr Gly Ser Leu Ser Ala Thr Gly Gln Pro Lys Phe
 130 135 140
 His Lys Gly Phe Glu Pro Leu Val Pro Gly Phe Ser Tyr Ala Lys Leu
 145 150 155 160
 Asn Asp Ile Asp Ser Val Tyr Lys Leu Leu Asp Glu Glu Thr Ala Gly
 165 170 175
 Ile Ile Ile Glu Val Ile Gln Gly Glu Gly Gly Val Asn Glu Ala Ser
 180 185 190
 Glu Asp Phe Leu Ser Lys Leu Gln Glu Ile Cys Lys Glu Lys Asp Val
 195 200 205
 Leu Leu Ile Ile Asp Glu Val Gln Thr Gly Ile Gly Arg Thr Gly Glu
 210 215 220
 Phe Tyr Ala Tyr Gln His Phe Asn Leu Lys Pro Asp Val Ile Ala Leu
 225 230 235 240
 Ala Lys Gly Leu Gly Gly Gly Val Pro Ile Gly Ala Ile Leu Ala Arg
 245 250 255
 Glu Glu Val Ala Gln Ser Phe Thr Pro Gly Ser His Gly Ser Thr Phe
 260 265 270
 Gly Gly Asn Pro Leu Ala Cys Arg Ala Gly Thr Val Val Val Asp Glu
 275 280 285
 Val Glu Lys Leu Leu Pro His Val Arg Glu Val Gly Asn Tyr Phe Lys
 290 295 300
 Glu Lys Leu Lys Glu Leu Gly Lys Gly Lys Val Lys Gly Arg Gly Leu
 305 310 315 320
 Met Leu Gly Leu Glu Leu Glu Arg Glu Cys Lys Asp Tyr Val Leu Lys
 325 330 335
 Ala Leu Glu Arg Asp Phe Ser
 340

- (2) INFORMATION FOR SEQ ID NO:29:
- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 398 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Arg Lys Leu Ala Glu Arg Ala Gln Lys Leu Ser Pro Ser Pro Thr
5 10 15

Leu Ser Val Asp Thr Lys Ala Lys Glu Leu Leu Arg Gln Gly Glu Arg
20 25 30

Val Ile Asn Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Glu His
35 40 45

Ile Lys Glu Ala Ala Lys Arg Ala Leu Asp Gln Gly Phe Thr Lys Tyr
50 55 60

Thr Pro Val Ala Gly Ile Leu Pro Leu Arg Glu Ala Ile Cys Glu Lys
65 70 75 80

Leu Tyr Arg Asp Asn Gln Leu Glu Tyr Ser Pro Asn Glu Ile Val Val
85 90 95

Ser Cys Gly Ala Lys His Ser Ile Phe Asn Ala Leu Gln Val Leu Leu
100 105 110

Asp Pro Gly Asp Glu Val Ile Ile Pro Val Pro Tyr Trp Thr Ser Tyr
115 120 125

Pro Glu Gln Val Lys Leu Ala Gly Gly Val Pro Val Phe Val Pro Thr
130 135 140

Ser Pro Glu Asn Asp Phe Lys Leu Arg Pro Glu Asp Leu Arg Ala Ala
145 150 155 160

Val Thr Pro Arg Thr Arg Leu Leu Ile Leu Asn Ser Pro Ala Asn Pro
165 170 175

Thr Gly Thr Val Tyr Arg Arg Glu Glu Leu Ile Gly Leu Ala Glu Val
180 185 190

Ala Leu Glu Ala Asp Leu Trp Ile Leu Ser Asp Glu Ile Tyr Glu Lys
195 200 205

Leu Ile Tyr Asp Gly Met Glu His Val Ser Ile Ala Ala Leu Asp Pro
210 215 220

Glu Val Lys Lys Arg Thr Ile Val Val Asn Gly Val Ser Lys Ala Tyr
225 230 235 240

Ala Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Ala Pro Arg Pro Ile
245 250 255

Ala Gln Ala Met Thr Asn Leu Gln Ser His Ser Thr Ser Asn Pro Thr
260 265 270

Ser Val Ala Gln Ala Ala Ala Leu Ala Ala Leu Lys Gly Pro Gln Glu
275 280 285

Pro Val Glu Asn Met Arg Arg Ala Phe Gln Lys Arg Arg Asp Phe Ile
290 295 300

Trp Gln Tyr Leu Asn Ser Leu Pro Gly Val Arg Cys Pro Lys Pro Leu
305 310 315 320

Gly Ala Phe Tyr Val Phe Pro Glu Val Glu Arg Ala Phe Gly Pro Pro
325 330 335

Ser Lys Arg Thr Gly Asn Thr Thr Ala Ser Asp Leu Ala Leu Phe Leu
340 345 350

Leu Glu Glu Ile Lys Val Ala Thr Val Ala Gly Ala Ala Phe Gly Asp
355 360 365

Asp Arg Tyr Leu Arg Phe Ser Tyr Ala Leu Arg Leu Glu Asp Ile Glu
370 375 380

Glu Gly Met Gln Arg Phe Lys Glu Leu Ile Glu Ala Ala Leu
385 390 395

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 592 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Cys Gly Ile Val Gly Tyr Val Gly Arg Asp Leu Ala Leu Pro Ile
5 10 15

Val Leu Gly Ala Leu Glu Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

Gly Val Ala Leu Ile Glu Asp Gly Lys Leu Ile Val Glu Lys Lys Lys
35 40 45

Gly Lys Ile Arg Glu Leu Val Lys Ala Leu Trp Gly Lys Asp Tyr Lys
50 55 60

Ala Lys Thr Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Lys Pro
65 70 75 80

Thr Asp Glu Asn Ala His Pro His Thr Asp Glu Lys Gly Glu Phe Ala
85 90 95

Val Val His Asn Gly Ile Ile Glu Asn Tyr Leu Glu Leu Lys Glu Glu
100 105 110

Leu Lys Lys Glu Gly Val Lys Phe Arg Ser Glu Thr Asp Thr Glu Val
115 120 125

Ile Ala His Leu Ile Ala Lys Asn Tyr Arg Gly Asp Leu Leu Glu Ala
130 135 140

Val Leu Lys Thr Val Lys Lys Leu Lys Gly Ala Phe Ala Phe Ala Val
145 150 155 160

Ile Thr Val His Glu Pro Asn Arg Leu Ile Gly Val Lys Gln Gly Ser
165 170 175

Pro Leu Ile Val Gly Leu Gly Glu Gly Glu Asn Phe Leu Ala Ser Asp
180 185 190

Ile Pro Ala Ile Leu Pro Tyr Thr Lys Lys Ile Ile Val Leu Asp Asp
 195 200 205
 Gly Glu Ile Ala Asp Leu Thr Pro Asp Thr Val Asn Ile Tyr Asn Phe
 210 215 220
 Glu Gly Glu Pro Val Ser Lys Glu Val Met Ile Thr Pro Trp Asp Leu
 225 230 235 240
 Val Ser Ala Glu Lys Gly Gly Phe Lys His Phe Met Leu Lys Glu Ile
 245 250 255
 Tyr Glu Gln Pro Lys Ala Ile Asn Asp Thr Leu Lys Gly Phe Leu Ser
 260 265 270
 Thr Glu Asp Ala Ile Pro Phe Lys Leu Lys Asp Phe Arg Arg Val Leu
 275 280 285
 Ile Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Phe Val Gly Lys Tyr
 290 295 300
 Trp Ile Glu Arg Phe Ala Gly Val Pro Thr Glu Val Ile Tyr Ala Ser
 305 310 315 320
 Glu Phe Arg Tyr Ala Asp Val Pro Val Ser Asp Lys Asp Ile Val Ile
 325 330 335
 Gly Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Lys Phe Ala Leu Gln
 340 345 350
 Ser Ala Lys Glu Lys Gly Ala Phe Thr Val Gly Leu Val Asn Val Val
 355 360 365
 Gly Ser Ala Ile Asp Arg Glu Ser Asp Phe Ser Leu His Thr His Ala
 370 375 380
 Gly Pro Glu Ile Gly Val Ala Ala Thr Lys Thr Phe Thr Ala Gln Phe
 385 390 395 400
 Thr Ala Leu Tyr Ala Leu Ser Val Arg Glu Ser Glu Glu Arg Glu Asn
 405 410 415
 Leu Ile Arg Leu Leu Glu Lys Val Pro Ser Leu Val Glu Gln Thr Leu
 420 425 430
 Asn Thr Ala Glu Glu Val Glu Lys Val Ala Glu Lys Tyr Met Lys Lys
 435 440 445
 Lys Asn Met Leu Tyr Leu Gly Arg Tyr Leu Asn Tyr Pro Ile Ala Leu
 450 455 460
 Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Gly
 465 470 475 480
 Tyr Pro Ala Gly Glu Met Lys His Gly Pro Ile Ala Leu Ile Asp Glu
 485 490 495
 Asn Met Pro Val Val Val Ile Ala Pro Lys Asp Arg Val Tyr Glu Lys
 500 505 510

Ile Leu Ser Asn Val Glu Glu Val Leu Ala Arg Lys Gly Arg Val Ile
515 520 525

Ser Val Gly Phe Lys Gly Asp Glu Thr Leu Lys Ser Lys Ser Glu Ser
530 535 540

Val Met Glu Ile Pro Lys Ala Glu Glu Pro Ile Thr Pro Phe Leu Thr
545 550 555 560

Val Ile Pro Leu Gln Leu Phe Ala Tyr Phe Ile Ala Ser Lys Leu Gly
565 570 575

Leu Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Thr Val Thr Val Glu
580 585 590

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 354 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Ile Pro Gln Arg Ile Lys Glu Leu Glu Ala Tyr Lys Thr Glu Val
5 10 15

Thr Pro Ala Ser Val Arg Leu Ser Ser Asn Glu Phe Pro Tyr Asp Phe
20 25 30

Pro Glu Glu Ile Lys Gln Arg Ala Leu Glu Glu Leu Lys Lys Val Pro
35 40 45

Leu Asn Lys Tyr Pro Asp Pro Glu Ala Lys Glu Leu Lys Ala Val Leu
50 55 60

Ala Asp Phe Phe Gly Val Lys Glu Glu Asn Leu Val Leu Gly Asn Gly
65 70 75 80

Ser Asp Glu Leu Ile Tyr Tyr Leu Ser Ile Ala Ile Gly Glu Leu Tyr
85 90 95

Ile Pro Val Tyr Ile Pro Val Pro Thr Phe Pro Met Tyr Glu Ile Ser
100 105 110

Ala Lys Val Leu Gly Arg Pro Leu Val Lys Val Gln Leu Asp Glu Asn
115 120 125

Phe Asp Ile Asp Leu Glu Arg Ser Ile Glu Leu Ile Glu Lys Glu Lys
130 135 140

Pro Val Leu Gly Tyr Phe Ala Tyr Pro Asn Asn Pro Thr Gly Asn Leu
145 150 155 160

Phe Ser Arg Gly Lys Ile Glu Glu Ile Arg Asn Arg Gly Val Phe Cys
165 170 175

Val Ile Asp Glu Ala Tyr Tyr His Tyr Ser Gly Glu Thr Phe Leu Glu
180 185 190

Asp Ala Leu Lys Arg Glu Asp Thr Val Val Leu Arg Thr Leu Ser Lys
 195 200 205
 Ile Gly Met Ala Ser Leu Arg Val Gly Ile Leu Ile Gly Lys Gly Glu
 210 215 220
 Ile Val Ser Glu Ile Asn Lys Val Arg Leu Pro Phe Asn Val Thr Tyr
 225 230 235 240
 Pro Ser Gln Val Met Ala Lys Val Leu Leu Thr Glu Gly Arg Glu Phe
 245 250 255
 Leu Met Glu Lys Ile Gln Glu Val Val Thr Glu Arg Glu Arg Met Tyr
 260 265 270
 Asp Glu Met Lys Lys Ile Glu Gly Val Glu Val Phe Pro Ser Lys Ala
 275 280 285
 Asn Phe Leu Leu Phe Arg Thr Pro Tyr Pro Ala His Glu Val Tyr Gln
 290 295 300
 Glu Leu Leu Lys Arg Asp Val Leu Val Arg Asn Val Ser Tyr Met Glu
 305 310 315 320
 Gly Leu Gln Lys Cys Leu Arg Val Ser Val Gly Lys Pro Glu Glu Asn
 325 330 335
 Asn Lys Phe Leu Glu Ala Leu Glu Glu Ser Ile Lys Ser Leu Ser Ser
 340 345 350
 Ser Leu

- (2) INFORMATION FOR SEQ ID NO:32:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 303 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Lys Pro Tyr Ala Lys Tyr Ile Trp Leu Asp Gly Arg Ile Leu Lys
 5 10 15
 Trp Glu Asp Ala Lys Ile His Val Leu Thr His Ala Leu His Tyr Gly
 20 25 30
 Thr Ser Ile Phe Glu Gly Ile Arg Gly Tyr Trp Asn Gly Asp Asn Leu
 35 40 45
 Leu Val Phe Arg Leu Glu Glu His Ile Asp Arg Met Tyr Arg Ser Ala
 50 55 60
 Lys Ile Leu Gly Ile Asn Ile Pro Tyr Thr Arg Glu Glu Val Arg Gln
 65 70 75 80
 Ala Val Leu Glu Thr Ile Lys Ala Asn Asn Phe Arg Glu Asp Val Tyr
 85 90 95

Ile Arg Pro Val Ala Phe Val Ala Ser Gln Thr Val Thr Leu Asp Ile
 100 105 110
 Arg Asn Leu Glu Val Ser Leu Ala Val Ile Val Phe Pro Phe Gly Lys
 115 120 125
 Tyr Leu Ser Pro Asn Gly Ile Lys Ala Thr Ile Val Ser Trp Arg Arg
 130 135 140
 Val His Asn Thr Met Leu Pro Val Met Ala Lys Ile Gly Gly Ile Tyr
 145 150 155 160
 Val Asn Ser Val Leu Ala Leu Val Glu Ala Arg Ser Arg Gly Phe Asp
 165 170 175
 Glu Ala Leu Leu Met Asp Val Asn Gly Tyr Val Val Glu Gly Ser Gly
 180 185 190
 Glu Asn Ile Phe Ile Val Arg Gly Gly Arg Leu Phe Thr Pro Pro Val
 195 200 205
 His Glu Ser Ile Leu Glu Gly Ile Thr Arg Asp Thr Val Ile Lys Leu
 210 215 220
 Ser Gly Asp Val Gly Leu Arg Val Glu Glu Lys Pro Ile Thr Arg Glu
 225 230 235 240
 Glu Val Tyr Thr Ala Asp Glu Val Phe Leu Val Gly Thr Ala Ala Glu
 245 250 255
 Ile Thr Pro Val Val Glu Val Asp Gly Arg Thr Ile Gly Thr Gly Lys
 260 265 270
 Pro Gly Pro Ile Thr Thr Lys Ile Ala Glu Leu Tyr Ser Asn Val Val
 275 280 285
 Arg Gly Lys Val Glu Lys Tyr Leu Asn Trp Ile Thr Pro Val Tyr
 290 295 300